RAW SEQUENCE LISTING ERROR REPORT
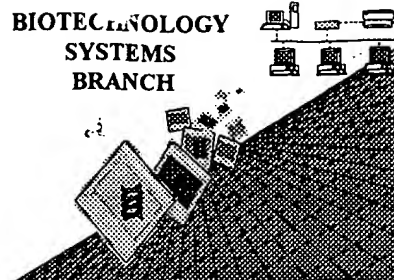
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/899,634_

Source: _OIPE_

Date Processed by STIC: _7/24/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/899,634

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line **not exceed 72 characters in length.** This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters,** instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If **intentional,** please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence *do not combine responses*

11 ____ Use of <220>

Sequence(s) 2,4 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/899,634   TIME: 10:14:58

Input Set : A:\Backup of SEQ IDs of application 4_31499A.wbk
Output Set: N:\CRF3\07242001\I899634.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Thomas Buehler, Reto Andreas Gadient, Reinhard Korn, Rao Movva
 4 <120> TITLE OF INVENTION: pCAR and its uses
 6 <130> FILE REFERENCE: 4-31499A
 8 <140> CURRENT APPLICATION NUMBER: US/09/899,634
 8 <141> CURRENT FILING DATE: 2001-07-05
 8 <160> NUMBER OF SEQ ID NOS: 4
10 <170> SOFTWARE: PatentIn version 3.0
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 4286
14 <212> TYPE: DNA
15 <213> ORGANISM: Artificial/Unknown
17 <220> FEATURE:
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20 <223> OTHER INFORMATION: delta pCAR gene
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28 agttgggatc tttgcattgg cccacggctc tcaggatggg gatgctcccc ttcagcaccc    180
30 ggttcccctt ggaaactgat ggtcctggct ctgtggcatg gcagtggcac tgtgaggagc    240
32 ccctaccagc agcacacagt gggtttggca ctgccacgct ccggatgccg cgctctgatc    300
34 caaccccata atcaagggaa cccgaattgc cccatcattg ccccaccac ccccatcctg    360
36 ccgggccctc acaccccacg ctgccttgtg gtgacattcc ccagcccaaa cccacggctt    420
38 catggctacc gcggggcatt tcccattgcc gccccattat cagctctgca cacctcccgc    480
40 tgtacccatg cctcgtggct gcccttcttt gacgtataat cttctaatta atacccggcc    540
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54 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct    960
56 gcaaagcccc tcgcagcgct gctcaccaac accgcgcacc gccccggccc agcctgcagc   1020
58 acgcgctgca aacaggaaag aaacaaaata ttgcccaaat gtaggcaaag gcattcggct   1080
60 gccttgacct ccgccgggcc gggccctgcc tgactcagct ccttactcag cgctcgcttc   1140
62 ctccctccgg ctgccaccgc cgcagcgcac accctgacaa agagtggccc ttaacgggct   1200
64 ctgaggtgca cccagcagtg cactcagcag tccaagggcc ggcctggagg tttgcaccgc   1260
66 tacgtgctga cattagcatt gaacttggcc ctgggtagtg ctgcaggccg ggcggggtgg   1320
68 gtgtagagag tgcagcgcgc gttgcacccg gtgccccttc ccctcccttg catcccagca   1380
70 ggctgcaccc cagcaccagg cccgtgcatg catgctcctg gtgttattgc agcctggtgc   1440
72 atgcatgcgt cttagtggtg cagcgctgtg catgcatcct ccttggtgtg tagcagctta   1500
74 gtgcatgcat acccctcggt gttattgctg ctctgtgcac gcacgctcat tgtatcactt   1560
76 catcccagtg catgcactca cactggagcg attgctgctc ggtgcacgca cactcattgt   1620
78 atcacgtcag ctcagtggct gcacgcacac cggtgttatt gctgctcggt gcgtgcatgc   1680
80 acatcagtgt cgctgcagct cagtgcatgc acgctcattg cccatcgcta tccctgcctc   1740
82 tcctgctggc gctccccggg aggtgacttc aaggggaccg caggaccacc tcgggggtgg   1800
84 ggggagggct gcacacgcgg accccgctcc ccctccccaa caaagcactg tggaatcaaa   1860
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 88 tgagccccac gttctgcttc actctcccca tctcccccccc ctccccaccc ccaattttgt   1980
 90 atttatttat tttttaatta ttttgtgcag cgatgggggc ggggggggg ggggcgcgcg   2040
 92 ccaggcgggg cggggcgggg cgaggggcgg ggcggggcga ggcggagagg tgcggcggca   2100
 94 gccaatcaga gcggcgcgct ccgaaagttt ccttttatgg cgaggcggcg gcggcggcgg   2160
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106 cccgcgctgc ccggcggctg tgagcgctgc gggcgcggcg cggggctttg tgcgctccgc   2520
108 gtgtgcgcga ggggagcgcg gccggggggcg gtgccccgcg gtgcggggggg gctgcgaggg   2580
110 gaacaaaggc tgcgtgcggg gtgtgtgcgt ggggggggtga gcaggggtg tgggcgcggc   2640
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122 aaatctggga ggcgccgccg cacccccctct agcgggcgcg ggcgaagcgg tgcggcgccg   3000
124 gcaggaagga aatgggcggg gagggccttc gtgcgtcgcc gcgccgccgt ccccttctcc   3060
126 atctccagcc tcggggctgc cgcagggggga cggctgcctt cggggggggac ggggcagggc   3120
128 ggggttcggc ttctggcgtg tgaccggcgg ggtttatatc ttcccttctc tgttcctccg   3180
130 cagccccccaa gcttaaggtg cacggcccac gtggggacta gtgccacc atg gcg ctc   3237
131                                                    Met Ala Leu
132                                                     1
134 ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc acc aga agt   3285
135 Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu Thr Arg Ser
136     5                   10                  15
138 ttg agt atc act act cct gaa cag atg att gaa aag gcc aaa ggg gaa   3333
139 Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala Lys Gly Glu
140 20                  25                  30                  35
142 act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa gac cag ggg   3381
143 Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu Asp Gln Gly
144                 40                  45                  50
146 ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat cag aag gtg   3429
147 Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn Gln Lys Val
148             55                  60                  65
150 gat caa gtg att att tta tat tct gga gac aaa att tat gac gac tac   3477
151 Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr Asp Asp Tyr
152         70                  75                  80
154 tac caa gat ctg aaa gga cga gta cat ttt aca agt aat gat ctc aaa   3525
155 Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn Asp Leu Lys
156     85                  90                  95
158 tca ggt gat gca tca ata aat gta aca aat cta cag ttg tca gat att   3573
159 Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu Ser Asp Ile
160 100                 105                 110                 115
162 ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt gga aat aag   3621
163 Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val Gly Asn Lys
164                 120                 125                 130
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167 Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr Arg Cys Tyr
168             135                 140                 145
170 gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta aaa tgt gaa    3717
171 Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu Lys Cys Glu
172             150                 155                 160
174 cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag aaa ttg tcc    3765
175 Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln Lys Leu Ser
176             165                 170                 175
178 aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg act tca cct    3813
179 Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met Thr Ser Pro
180 180             185                 190                 195
182. gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg aca tac agc    3861
183 Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly Thr Tyr Ser
184             200                 205                 210
186 tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg ctt cgc ctg    3909
187 Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu Leu Arg Leu
188             215                 220                 225
190 gat gtg gtt cct cct tca aat aga gct gga aca att gca gga gct gtt    3957
191 Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala Gly Ala Val
192             230                 235                 240
194 ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt atc atc ttt tgc    4005
195 Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile Ile Phe Cys
196             245                 250                 255
198 tgt cgt taa tctagataag taatgatcat aatcagccat atcacatctg           4054
199 Cys Arg
200 260
202 tagaggtttt acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa  4114
204 tgaatgcaat tgttgttgtt aacttgttta ttgcagctta taatggttac aaataaagca  4174
206 atagcatcac aaatttcaca aataaagcat tttttcact gcattctagt tgtggtttgt   4234
208 ccaaactcat caatgtatct tatcatgtct ggatccccgg gtaccgagct cg          4286
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213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial/Unknown
216 <220> FEATURE:
216 <223> OTHER INFORMATION:
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223             20                 25                 30
226 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
227             35                 40                 45
230 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
231 50                 55                 60
234 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
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C--> 214 <213> ORGANISM: Artificial/Unknown

W--> 216 <220> FEATURE:

W--> 216 <223> OTHER INFORMATION:

item 10

see item 11 on Erra Summary Sheet

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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242 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
243              100            105            110
246 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
247          115            120            125
250 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
251      130            135            140
254 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
255 145            150            155            160
258 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
259              165            170            175
262 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
263              180            185            190
266 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
267          195            200            205
270 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
271      210            215            220
274 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
275 225            230            235            240
278 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
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293 <222> LOCATION: (1)..(1098)
294 <223> OTHER INFORMATION: full length porcine CAR
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300 1              5              10              15
302 acc aga agt ttg agt atc act act cct gaa cag atg att gaa aag gcc      96
303 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
304              20              25              30
306 aaa ggg gaa act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa     144
307 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
308          35              40              45
310 gac cag ggg ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat     192
311 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
312      50              55              60
314 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat     240
315 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
316 65              70              75              80
318 gac gac tac tac caa gat ctg aaa gga cga gta cat ttt aca agt aat     288
319 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
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RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/899,634   TIME: 10:14:58

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Output Set: N:\CRF3\07242001\I899634.raw

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324                    100                  105                  110
326 tca gat att ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt     384
327 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
328                    115                  120                  125
330 gga aat aag aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca     432
331 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
332       130                  135                  140
334 aga tgt tat gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta     480
335 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
336 145                  150                  155                  160
338 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag     528
339 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
340                    165                  170                  175
342 aaa ttg tcc aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg     576
343 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
344                    180                  185                  190
346 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg     624
347 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
348                    195                  200                  205
350 aca tac agc tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg     672
351 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
352       210                  215                  220
354 ctt cgc ctg gat gtg gtt cct cct tca aat aga gct gga aca att gca     720
355 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
356 225                  230                  235                  240
358 gga gct gtt ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt att     768
359 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
360                    245                  250                  255
362 gtg ttt tgc tgt cat aaa aag cgc aga gaa gaa aaa tac gaa aaa gaa     816
363 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu
364                    260                  265                  270
366 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga acg     864
367 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr
368       275                  280                  285
370 tcc act gcc aga agc tac ctc ggc agc aac cac tcg tcc ctg gga tcc     912
371 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser
372       290                  295                  300
374 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag     960
375 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln
376 305                  310                  315                  320
378 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg     1008
379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro
380                    325                  330                  335
382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct     1056
383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro
384                    340                  345                  350
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VERIFICATION SUMMARY   DATE: 07/24/2001
PATENT APPLICATION: **US/09/899,634**   TIME: 10:14:59

Input Set : **A:\Backup of SEQ IDs of application 4_31499A.wbk**
Output Set: **N:\CRF3\07242001\I899634.raw**

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L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:214 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:216 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:216 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:396 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:396 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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